lalign output for seq id no. 9 vs. CDC4 (X05625)

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EXHIBIT A

x **lalign output for seq id no. 9 vs. CDC4 (X05625)**

[ISREC-Server] Date: Mon Feb 4 19:46:27 Europe/Zurich 2008

LALIGN finds the best local alignments between two sequences version 2.0u66 September 1998 Please cite: X. Huang and W. Miller (1991) Adv. Appl. Math. 12:373-381 resetting to DNA matrix

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Comparison of:
(A) ./wwwtmp/lalign/.7956.1.seq seq id no. 9                               - 2076 n
(B) ./wwwtmp/lalign/.7956.2.seq CDC4 (X05625)                              - 2954 n
 using matrix file: DNA, gap penalties: -14/-4

  56.3% identity in 350 nt overlap; score:  173 E(10,000): 3.9e-05

        1360      1370      1380      1390      1400      1410
seq   TCCCCTG-CCTGGTACAAAGAA-AAGCAAAAGAATT-TACGAAGATTGTGATCTCTTAT
      : :: ::: :::    :: :::: ::::: :::::  :  :: :::::  : ::
CDC4  TACCATGACCTTTCCCAGAGAATAAGCATT--GACTCATACTTAGATAAT-ATAGCTTAA
        2630      2640      2650      2660      2670

        1420      1430      1440      1450      1460      1470
seq   TAAATCAATTGT-TACTGATCATGAATGTT-AGTTAGAAAATGTTAGGTTTTAACTTAAA
      :::: : ::: : :: :  :  :: :: :  :   ::::   : :::::::  : ::
CDC4  TAAGT-AGTTATATAATCAGTAAAAAAGTACAATAACAACTTCGTACATTTTAT-TGAAT
    2680      2690      2700      2710      2720      2730

          1480                1490      1500      1510
seq   AAAAATTGTA----------TTGTGATTTTCAATTTTA----TGTTGA---AATCGGTGT
      : ::: :: :          :::: :: ::::::::::  :::: :  :: :::
CDC4  ATAAACTGCAGCTAAACTGCTTGT-ATGTTCAATTTTAATTGTTTTACAAAAAGGGTGC
    2740      2750      2760      2770      2780      2790

        1520      1530      1540      1550      1560      1570
seq   AGTATCCTGAGGTTTTTTTCCCCCCGAGAAGATAAAGAGGATAG-ACAACCTCTTAAAATA
      :: : : :  :  :::::  ::: ::: ::: :::  :::: :: ::::: ::
CDC4  CGTTTATTAATTAATGTTTCTTCCCTGAAAATAT---GGAAAGTACAAGTTTTTAG----
    2800      2810      2820      2830      2840

        1580      1590      1600      1610      1620      1630
seq   TTTTTACAATTTAATGAGAAAAAGTTTAAAAT--TCTCAATACAAATCAAACAATTTAAA
      :: : ::: : ::::: :: ::::: :: :   :: :::::   : :
CDC4  --TTGAGAAGGGTTTAAGAAAGTTTTGAAAATGATCTAAAAAAATATAAAAGCAATCAAA
    2850      2860      2870      2880      2890      2900

        1640      1650      1660      1670      1680
seq   TATTTTTAAGAAAAAA-GGAAAAGTAGATAGTGATACTGAGGGTAAAAAAA
      :    :: :::: :::::::: : :  :  : :   :::
CDC4  GA----AATAAAAGCTGGAAAAATGCGTAATA--ACCGAAGTGACTAAAA
        2910      2920      2930      2940      2950

  56.8% identity in 183 nt overlap; score:  124 E(10,000):  0.48

        1470      1480      1490      1500      1510      1520
seq   ACTTAAAAAAAATTGTATTGTGATTTTCAATTTT--ATGTTGAAATCGGTGTAGTATCC-
      :::: :::::: : :::: :::: ::::  : ::    :  : :: :   ::: : :::::
```

EXHIBIT A

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CDC4   ACTTCAAAAATTTATTATTTAGATT---AGTTGCCAACATGGATAGGAGTGAACTATCCG
           1020      1030      1040      1050      1060      1070

              1530      1540      1550      1560      1570
seq    ---TGAGGTTTTTTTCCCCCCAGAAGATAAAGAGGATAGACAACCTCTTAAAATATTTTT
          ::   :: :::  :    :  : ::  :::::::::   :::      :  : : :::
CDC4   ACTTGGGGACTTTAATCAAGGATAATTTAAAGAGG---GAC-----CTAATAACGTCTTT
           1080      1090      1100              1110      1120

   1580      1590      1600      1610      1620      1630
seq    ACAATTTAATGAGAAAAAGTTT-AAAATTCTCAATA-----CAAATCAAACAATTTAAAT
          :  ::: :     :: ::::::: ::::::: :::::         ::: :: :   : ::: :
CDC4   GCCTTTTGA----AATAAGTTTGAAAATTTTCAATTATTTGCAATTCGAGGATATTATAA
           1130      1140      1150      1160      1170


seq    ATT
       :::
CDC4   ATT
       1180
```

```
 55.0% identity in 269 nt overlap;  score:  116 E(10,000):    2.2

          1170      1180      1190      1200      1210      1220
seq    CATTGAAAAAGAACGAAAGCCTCAAAGCCTGTATTCGCTGTAAT-TCACCTGCAA--AAT
       ::  :  ::::::: ::  :  :  :      :  : :::   :   ::: : : ::::::    ::
CDC4   CAGTAAAAAAGTACAATAACAACT--TCGTACATTTTATTGAATATAAACTGCAGCTAAA
           2700      2710      2720      2730      2740      2750

          1230      1240      1250      1260      1270      1280
seq    ATGATTGCTATTTACAACGGGCAACCTGCAAACGAGAAGGCTGTGGATTTGATTATTGTA
       :: ::: ::: : :::      :       :   : ::  ::      ::  :: ::::: : :
CDC4   CTGCTTG-TATGTTCAATTTTAATTGTGTTTACAAAAAGG--GTGCCGTTTATTAATTAA
           2760      2770      2780      2790      2800

          1290      1300      1310      1320      1330
seq    CGAAGTGTCTCTGTAATTATC-ATACTACTAAAGACTGTTCAGATGGCAAGCTCCTCAAA
       :      :: ::: :: ::: : : :::  : : : :::  ::  :: :: :::      : :
CDC4   TGTTTCTTCCCTGAAAATATGGAAAGTAC--AAG--TTTTTAGTTGAGAAGG--GTTTAA
       2810      2820      2830      2840      2850      2860

       1340      1350      1360      1370      1380      1390
seq    GCCAGTTGTAAAATAGGTCCCCTGCCTGGTACAA-AGAAAAGCAA--AAAGAATTTACGA
       :  :::::  : ::: :  :: ::       :  :: ::: ::::::::::  ::::: : :  :
CDC4   GAAAGTTTTGAAAATGATC-------TAAAAAAATAAAAGCAATCAAAGAAATAA--A
           2870      2880              2890      2900      2910

       1400      1410      1420
seq    AGATTGTGATCT-CTTATTAAATCAATTG
       :: :: :  :  :  :: ::: :::    :: ::
CDC4   AGCTGGAAAAATGCGTAATAACCGAAGTG
           2920      2930      2940
```

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EXHIBIT A

☒ **lalign output for seq id no. 9 vs. Grr1 (M59247**

[ISREC-Server] Date: Mon Feb 4 19:51:18 Europe/Zurich 2008

LALIGN finds the best local alignments between two sequences version 2.0u66 September 1998 Please cite: X. Huang and W. Miller (1991) Adv. Appl. Math. 12:373-381 resetting to DNA matrix

```
 Comparison of:
(A) ./wwwtmp/lalign/.20359.1.seq seq id no. 9                              - 2076
(B) ./wwwtmp/lalign/.20359.2.seq Grr1 (M59247                              - 4470
 using matrix file: DNA, gap penalties: -14/-4

  54.4% identity in 522 nt overlap; score:  128 E(10,000):   0.34

     1160      1170      1180      1190      1200      1210
seq  AAGACATTGAAAAAGAACGAA-AGC-CTCAAAGCCTGTATTCGCTGTAATTCACCTGCAA
     :: :::: : :: : :::  ::: :: : :: :: :: : : :::  : :::
Grr1 AAAATATTAACAATTATAGAAGAGTACAAAAAGTCATTATATGCA-TACTGCCATTCCAA
     1210      1220      1230      1240      1250      1260

     1220      1230      1240      1250      1260      1270
seq  AATATGATTGCTATTTACAACGGGCAACCTGCAAACGAGAAGGCTGTGGATTTGATTATT
     :: ::: :   :::: : : :: :::::  :: ::  : :: :
Grr1 GCTAAGAGGTCA----ACAA-GTGGAAAATCCAACAGATAATT-TCATCATTTGGATAAA
     1270      1280      1290      1300      1310      1320

     1280      1290      1300      1310      1320      1330
seq  GTACGAAGTGTCT-CTGTAATTATCATACTACTAAAGACTG--TTCA-GATGG--CAAGC
     : : ::   :: ::: ::: ::: :::  :::::  : : :::  : ::
Grr1 CTCCATAGATACTACTG-AATCATCTGACTTG-AAAGAAGGGCTACAAGATCTTTCGAGA
       1330      1340      1350      1360      1370      1380

     1340      1350      1360      1370      1380
seq  TCCTCAAAGCCAGTTGTAAAATAG-GTCCCCT-GCCTGGTACAAAGAAAAGCAAA---AA
     : : :::: :: :::: : :::::  :::: : :: :   :::: ::: :: :    :
Grr1 TATTCAAGGC-AGTTCATAAATAATGTGCTTTCGAATCCATCAAATCAAAACATATGTAC
           1390      1400      1410      1420      1430

     1390      1400      1410      1420      1430
seq  GAATTTA---CGAAGAT----TGTGATCTCTTATTAAATCAATTGTTACTGATCATGAAT
     :: : :  ::::::: :  ::: : : : :::  ::::: :::  :: :  :::
Grr1 GAGTGTCCACCCGAAGATCACCTGTGTTTGCCC--TAAA-CA--TGCTACCC-TCGGAAAT
     1440      1450      1460      1470      1480      1490

     1440      1450      1460      1470      1480      1490
seq  GTTAGTTAGAAAATGTTAGGTTTTAACTTAA---AAAAAATTGTATTGTGATTTTCAATT
     ::: :  :: :::: :   ::::::: :  :::::::  : :: : :: ::
Grr1 ATTAC--ACTTAATTATTAGATA--AACTTAACCAAAAATATGATATTGTAAAATTCCTTA
         1500      1510      1520      1530      1540

     1500      1510      1520      1530      1540
seq  TTATGTTGAAA-TCGG---TGTAGTA-TCCTGAGGTTTTTTT--------CCCCCCAG-A
     : : ::: ::: :: ::   :: : :::: ::: : ::  :::      :: : :: :
Grr1 CCGTTTCCAAACTCTGGGCTGAAATAATTGTGAAGATACTTTTATTACAGACCGCACATCA
     1550      1560      1570      1580      1590      1600
```

EXHIBIT A

```
        1550      1560      1570      1580      1590
seq  AGATAAAGAGGA---TAGACAACCTCTTAA--AATATTTTTACAATTTAATGAGAAAAAG
     : :  :::::::   :::::   : :::: : :::    :: ::   :::::  :
Grr1 ACAAAAAGAGTCAATTAGACTTGTTTTTAAGGACTATGAAGTTAACTTCTGAAGAAACTG
     1610      1620      1630      1640      1650      1660


      1600      1610      1620      1630
seq  TTTAAAATTCTCAATACAA-ATCAAACAATTTAAATATTTTA
     : :  :: :: :: :  :  :::::: : ::::::  ::: ::
Grr1 TATTCAACTATCGTTTAATGATCAAA-AGATTAAATTTTTCA
     1670      1680      1690      1700      1710
```

55.5% identity in 229 nt overlap; score: 117 E(10,000):   2.8

```
      1290      1300      1310      1320      1330      1340
seq  TCTGTAATTATCATACTACTAAAGACTGTTCAGATG-GCAAGCTCCTCAAAGCCAGTTGT
     : ::  ::: :  :: :::   :::  :::  ::::: : :: :::: ::  :  :  ::
Grr1 TTTGGCAATAGAATGCAAATATCACCTGACCAGATGAGGAATCTCCA-AATGGGACTTCG
     3810      3820      3830      3840      3850      3860


      1350      1360      1370      1380      1390      1400
seq  AAAATAGGTCCCCTGCCTGGTACAAAGAAAAGCAAAAAGAATTTACGAAG-ATTG--TGA
     ::    :: :   ::  : : :  ::: ::: :  :: :::  :::: :: ::   :: :
Grr1 TAATCAGAACA--TGGTTAGGAACAATAACAACAACAC-AATTGACGAATCAATGCCTGA
     3870      3880      3890      3900      3910


      1410      1420      1430      1440      1450
seq  T-CTCTTATTAAATC---AATTGTTACTG-ATCATGAATGTTAGTTAGAAA-ATGTTAGG
     ::   ::: : ::  ::: :::: ::: :   : ::::: :: ::::: :::: :: :::
Grr1 CACTGCCATTGATTCTCAAATGGATGAAGCATCAGGAACGCCCGATGAAGATATGTTATA
     3920      3930      3940      3950      3960      3970


   1460      1470      1480      1490      1500
seq  TTTTAACTTAAAAAAAATTGTATTGTGATTTT-CAATTTTATGTTGAAA
     ::  : ::: :  :::    :: ::: : :::  ::: :: :::::: :: :::
Grr1 ATTGTATTTCATTGAATACTTACTGTCCTACTACACCTTTATTTTCAAA
     3980      3990      4000      4010      4020
```

56.3% identity in 199 nt overlap; score: 112 E(10,000):   7.3

```
      1880      1890      1900      1910      1920      1930
seq  TTTCCCAAGAAAGTATCCTTTGTAAAAACTTGCTTGTTTTCCTTATTTCTGAAATCTGTT
     : ::  ::::: :   :   : ::  : :::::::::::  :   :::: ::    :::::
Grr1 TGTTCCAATTATCGAAGCTGGGCAAAAACTTGCAAACAGTGC--ATTT-TGGGCACTGTT
     2380      2390      2400      2410      2420


      1940      1950      1960      1970      1980      1990
seq  TTAATATTTTTGTATACATGTAAATATTTCTGTGATTTTTTATATGTCAAAGAATAT-GTC
     : ::::: :   ::   ::  :  :: ::  :: : ::: ::  : :::: :::::::::  ::
Grr1 TCAATATAACTGATAACGGGGTAAGAGCACTCT--TTCATTCATGTACAAGAATACAGTA
     2430      2440      2450      2460      2470      2480


              2000      2010      2020      2030      2040
seq  T-----CTT---GTA-TGTAC--ATATAAA-AATAAATTTTGCTCAATAAAATTGTAAGC
     :       ::: ::  ::::::  :: ::: ::: :  : ::::: :: :::  :::
Grr1 TGTGGACTTTGCGTGCGTGTACGAATTTAACCAATAGAACT--CTTTATGAACTAGCAGAC
     2490      2500      2510      2520      2530      2540
```

---

lalign output for seq id no. 9 vs. Grr1 (M59247

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EXHIBIT A

```
        2050      2060
seq     TTAAAAAAAAAAAAAAAAA
        :::  ::::  :::  :  ::
Grr1    TTACCAAAATTAAAGAGAA
        2550      2560
```

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